



1  
SEQUENCE LISTING

<110> RONALD M.  
NO, DAVID  
SAEZ, ENRIQUE

*Sub*  
*E*  
<120> METHODS FOR MODULATING EXPRESSION OF EXOGENOUS GENES IN MAMMALIAN SYSTEMS, AND PRODUCTS RELATED THERETO

<130> SALK1520-2

<140> 09/042,488  
<141> 1998-03-16

<150> 08/974,530  
<151> 1997-11-19

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<170> PatentIn Ver. 2.1

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20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys  
35 40 45

Xaa Xaa Xaa Lys Xaa Xaa Arg Xaa Xaa Cys Xaa Xaa Cys Arg Xaa Xaa  
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Lys Cys Xaa Xaa Xaa Gly Met  
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ggc gag gac gtg gcg atg gcg cat gcc gac gcg cta gac gat ttc gat	96
Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp	
20 25 30	
ctg gac atg ttg ggg gac ggg gat tcc ccg ggt ccg gga ttt acc ccc	144
Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro	
35 40 45	
cac gac tcc gcc ccc tac ggc gct ctg gat atg gcc gac ttc gag ttt	192
His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe	
50 55 60	
gag cag atg ttt acc gat gcc ctt gga att gac gag tac ggt ggg aag	240
Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys	
65 70 75 80	
ctt cta ggt acc tct aga agg ata tcg aat tct ata tct tca ggt cgc	288
Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg	
85 90 95	
gat gat ctc tcg cct tcg agc agc ttg aac gga tac tcg gcg aac gaa	336
Asp Asp Leu Ser Pro Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu	
100 105 110	
agc tgc gat gcg aag aag agc aag aag gga cct gcg cca cgg gtg caa	384
Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln	
115 120 125	
gag gag ctg tgc ctg gtt tgc ggc gac agg gcc tcc ggc tac cac tac	432
Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr	
130 135 140	
aac gcc ctc acc tgt gga tcc tgc aag gtg ttc ttt cga cgc agc gtt	480
Asn Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Arg Arg Ser Val	
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Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met	
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gac atg tac atg agg cga aag tgt cag gag tgc cgc ctg aaa aag tgc	576
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180 185 190	
ctg gcc gtg ggt atg cggt ccg gaa tgc gtc gtc ccg gag aac caa tgt	624
Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys	
195 200 205	

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ggt ggc ggc caa gac ttt gtt aag aag gag att ctt gac ctt atg aca Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr 245 250 255	768
tgc gag ccg ccc cag cat gcc act att ccg cta cta cct gat gaa ata Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile 260 265 270	816
ttg gcc aag tgt caa gcg cgc aat ata cct tcc tta acg tac aat cag Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln 275 280 285	864
ttg gcc gtt ata tac aag tta att tgg tac cag gat ggc tat gag cag Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln 290 295 300	912
cca tct gaa gag gat ctc agg cgt ata atg agt caa ccc gat gag aac Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn 305 310 315 320	960
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ctc acg gtc cag ttg att gtt gag ttt gct aaa ggt cta cca gcg ttt Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe 340 345 350	1056
aca aag ata ccc cag gag gac cag atc acg tta cta aag gcc tgc tcg Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser 355 360 365	1104
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gac tca ata ttc ttc gcg aat aat aga tca tat acg cgg gat tct tac Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr 385 390 395 400	1200
aaa atg gcc gga atg gct gat aac att gaa gac ctg ctg cat ttc tgc Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys 405 410 415	1248
cgc caa atg ttc tcg atg aag gtg gac aac gtc gaa tac gcg ctt ctc Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu 420 425 430	1296

act gcc att gtg atc ttc tcg gac cgg ccg ggc ctg gag aag gcc caa		1344	
Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln			
435	440	445	
cta gtc gaa gcg atc cag agc tac tac atc gac acg cta cgc att tat		1392	
Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr			
450	455	460	
ata ctc aac cgc cac tgc ggc gac tca atg agc ctc gtc ttc tac gca		1440	
Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala			
465	470	475	480
aag ctg ctc tcg atc ctc acc gag ctg cgt acg ctg ggc aac cag aac		1488	
Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn			
485	490	495	
gcc gag atg tgt ttc tca cta aag ctc aaa aac cgc aaa ctg ccc aag		1536	
Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys			
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ttc ctc gag gag atc tgg gac gtt cat gcc atc ccg cca tcg gtc cag		1584	
Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln			
515	520	525	
tcg cac ctt cag att acc cag gag gag aac gag cgt ctc gag cgg gct		1632	
Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala			
530	535	540	
gag cgt atg cgg gca tcg gtt ggg ggc gcc att acc gcc ggc att gat		1680	
Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp			
545	550	555	560
tgc gac tct gcc tcc act tcg gcg gca gcc gcg gcc cag cat cag		1728	
Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln			
565	570	575	
cct cag cct cag ccc cag ccc caa ccc tcc tcc ctg acc cag aac gat		1776	
Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp			
580	585	590	
tcc cag cac aca cag ccg cag cta caa cct cag cta cca cct cag		1824	
Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln			
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ctg caa ggt caa ctg caa ccc cag ctc caa cca cag ctt cag acg caa		1872	
Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln			
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ctc cag cca cag att caa cca cag cca cag ctc ctt ccc gtc tcc gct		1920	
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Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser			
645	650	655	

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660 665 670	
ccg gca acc acc agc agt atc acg gct gcc gtt acc gct agc tcc acc Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr	2064
675 680 685	
aca tca gcg gta ccg atg ggc aac gga gtt gga gtc ggt gtt ggg gtg Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val	2112
690 695 700	
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705 710 715 720	
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His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe 50 55 60	
Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys 65 70 75 80	
Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg 85 90 95	
Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu 100 105 110	
Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln 115 120 125	

Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr  
 130 135 140  
 Asn Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Arg Arg Ser Val  
 145 150 155 160  
 Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met  
 165 170 175  
 Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys  
 180 185 190  
 Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys  
 195 200 205  
 Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met  
 210 215 220  
 Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser  
 225 230 235 240  
 Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr  
 245 250 255  
 Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile  
 260 265 270  
 Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln  
 275 280 285  
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 290 295 300  
 Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn  
 305 310 315 320  
 Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile  
 325 330 335  
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 340 345 350  
 Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser  
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 Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser  
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 385 390 395 400  
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 405 410 415  
 Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu  
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Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln  
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Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn  
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Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys  
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Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln  
515 520 525

Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala  
530 535 540

Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp  
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Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln  
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Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln  
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Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln  
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Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala  
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Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser  
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Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr  
660 665 670

Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr  
675 680 685

Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val  
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Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu  
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ctg gac atg ttg ggg gac ggg gat tcc ccg ggt ccg gga ttt acc ccc 144  
Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro  
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cac gac tcc gcc ccc tac ggc gct ctg gat atg gcc gac ttc gag ttt 192  
 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe  
       50                 55                 60

gag cag atg ttt acc gat gcc ctt gga att gac gag tac ggt ggg aag 240  
Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys  
65 70 75 80

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ctt cta ggt acc tct aga agg ata tcg aat tct ata tct tca ggt cgc  288
Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg
          85           90           95

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gat gat ctc tcg cct tcg agc agc ttg aac gga tac tcg gcg aac gaa 336
Asp Asp Leu Ser Pro Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu
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agc tgc gat gcg aag aag agc aag aag gga cct gcg cca cgg gtg caa      384
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aac gcc ctc acc tgt gag ggc tgc aag ggg ttc ttt cga cgc agc gtt 480
Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val
145          150          155          160

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acg aag agc gcc gtc tac tgc tgc aag ttc ggg cgc gcc tgc gaa atg		528	
Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met			
165	170	175	
gac atg tac atg agg cga aag tgt cag gag tgc cgc ctg aaa aag tgc		576	
Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys			
180	185	190	
ctg gcc gtg ggt atg cgg ccg gaa tgc gtc gtc ccg gag aac caa tgt		624	
Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys			
195	200	205	
gcg atg aag cgg cgc gaa aag aag gcc cag aag gag aag gac aaa atg		672	
Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met			
210	215	220	
acc act tcg ccg agc tct cag cat ggc ggc aat ggc agc ttg gcc tct		720	
Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser			
225	230	235	240
ggt ggc ggc caa gac ttt gtt aag aag gag att ctt gac ctt atg aca		768	
Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr			
245	250	255	
tgc gag ccg ccc cag cat gcc act att ccg cta cta cct gat gaa ata		816	
Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile			
260	265	270	
ttg gcc aag tgt caa gcg cgc aat ata cct tcc tta acg tac aat cag		864	
Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln			
275	280	285	
ttg gcc gtt ata tac aag tta att tgg tac cag gat ggc tat gag cag		912	
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Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn			
305	310	315	320
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Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile			
325	330	335	
ctc acg gtc cag ttg att gtt gag ttt gct aaa ggt cta cca gcg ttt		1056	
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355	360	365	
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Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser			
370	375	380	

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aaa atg gcc gga atg gct gat aac att gaa gac ctg ctg cat ttc tgc Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys 405 410 415	1248
cgc caa atg ttc tcg atg aag gtg gac aac gtc gaa tac g <sup>c</sup> gtt ctc Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu 420 425 430	1296
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gcc gag atg tgt ttc tca cta aag ctc aaa aac cgc aaa ctg ccc aag Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys 500 505 510	1536
t <sup>c</sup> tc ctc gag gag atc tgg gac gtt cat gcc atc ccg cca tcg gtc cag Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln 515 520 525	1584
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gag cgt atg cgg gca tcg gtt ggg ggc gcc att acc gcc ggc att gat Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp 545 550 555 560	1680
tgc gac tct gcc tcc act tcg gcg gca gcc g <sup>c</sup> g <sup>c</sup> cag cat cag Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln 565 570 575	1728
cct cag cct cag ccc cag ccc caa ccc tcc tcc ctg acc cag aac gat Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp 580 585 590	1776
tcc cag cac cag aca cag ccg cag cta caa cct cag cta cca cct cag Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln 595 600 605	1824

ctg caa ggt caa ctg caa ccc cag ctc caa cca cag ctt cag acg caa Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln 610 615 620	1872
ctc cag cca cag att caa cca cag cca cag ctc ctt ccc gtc tcc gct Leu Gln Pro Gln Ile Gln Pro Gln Leu Leu Pro Val Ser Ala 625 630 635 640	1920
ccc gtg ccc gcc tcc gta acc gca cct ggt tcc ttg tcc gcg gtc agt Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser 645 650 655	1968
acg agc agc gaa tac atg ggc gga agt gcg gcc ata gga ccc atc acg Thr Ser Ser Glu Tyr Met Gly Ser Ala Ala Ile Gly Pro Ile Thr 660 665 670	2016
ccg gca acc acc agc agt atc acg gct gcc gtt acc gct agc tcc acc Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr 675 680 685	2064
aca tca gcg gta ccg atg ggc aac gga gtt gga gtc ggt gtt ggg gtg Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val 690 695 700	2112
ggc ggc aac gtc agc atg tat gcg aac gcc cag acg gcg atg gcc ttg Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu 705 710 715 720	2160
atg ggt gta gcc ctg cat tcg cac caa gag cag ctt atc ggg gga gtg Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val 725 730 735	2208
gcg gtt aag tcg gag cac tcg acg act gca tag Ala Val Lys Ser Glu His Ser Thr Thr Ala 740 745	2241

<210> 7  
<211> 746  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Recombinant  
VpEcR

<400> 7  
Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp  
1 5 10 15  
Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp  
20 25 30  
Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro  
35 40 45  
His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe  
50 55 60

Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Gly Lys  
 65 70 75 80

Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg  
 85 90 95

Asp Asp Leu Ser Pro Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu  
 100 105 110

Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln  
 115 120 125

Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr  
 130 135 140

Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val  
 145 150 155 160

Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met  
 165 170 175

Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys  
 180 185 190

Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys  
 195 200 205

Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met  
 210 215 220

Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser  
 225 230 235 240

Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr  
 245 250 255

Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile  
 260 265 270

Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln  
 275 280 285

Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln  
 290 295 300

Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn  
 305 310 315 320

Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile  
 325 330 335

Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe  
 340 345 350

Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser  
 355 360 365

Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser  
 370 375 380  
 Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr  
 385 390 395 400  
 Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys  
 405 410 415  
 Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu  
 420 425 430  
 Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln  
 435 440 445  
 Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr  
 450 455 460  
 Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala  
 465 470 475 480  
 Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn  
 485 490 495  
 Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys  
 500 505 510  
 Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln  
 515 520 525  
 Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala  
 530 535 540  
 Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp  
 545 550 555 560  
 Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln  
 565 570 575  
 Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp  
 580 585 590  
 Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu Pro Pro Gln  
 595 600 605  
 Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu Gln Thr Gln  
 610 615 620  
 Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro Val Ser Ala  
 625 630 635 640  
 Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser Ala Val Ser  
 645 650 655  
 Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly Pro Ile Thr  
 660 665 670

Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala Ser Ser Thr  
675 680 685

Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly Val Gly Val  
690 695 700

Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu  
705 710 715 720

Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile Gly Gly Val  
725 730 735

Ala Val Lys Ser Glu His Ser Thr Thr Ala  
740 745

```
<210> 8
<211> 3126
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Recombinant  
GEcR

<220>  
<221> CDS  
<222> (1) . . (3123)

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<400> 8
atg gac tcc aaa gaa tca tta act cct ggt aga gaa gaa aac ccc agc    48
Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser
          1           5           10          15

```

agt gtg ctt gct cag gag agg gga gat gtg atg gac ttc tat aaa acc 96  
Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr  
20 25 30

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cta aga gga gga gct act gtg aag gtt tct gcg tct tca ccc tca ctg      144
Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
          35           40           45

```

gct gtc gct tct caa tca gac tcc aag cag cga aga ctt ttg gtt gat 192  
Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp  
50 55 60

```

ttt cca aaa ggc tca gta agc aat gcg cag cag cca gat ctg tcc aaa 240
Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
   65           70           75           80

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gca gtt tca ctc tca atg gga ctg tat atg gga gag aca gaa aca aaa 288
Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
                    85          90          95

```

gtg atg gga aat gac ctg gga ttc cca cag cag ggc caa atc agc ctt 336  
Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu  
100 105 110

tcc tcg ggg gaa aca gac tta aag ctt ttg gaa gaa agc att gca aac		384
Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn		
115 120 125		
ctc aat agg tcg acc agt gtt cca gag aac ccc aag agt tca gca tcc		432
Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser		
130 135 140		
act gct gtg tct gct gcc ccc aca gag aag gag ttt cca aaa act cac		480
Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His		
145 150 155 160		
tct gat gta tct tca gaa cag caa cat ttg aag ggc cag act ggc acc		528
Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr		
165 170 175		
aac ggt ggc aat gtg aaa ttg tat acc aca gac caa agc acc ttt gac		576
Asn Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp		
180 185 190		
att ttg cag gat ttg gag ttt tct tct ggg tcc cca ggt aaa gag acg		624
Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr		
195 200 205		
aat gag agt cct tgg aga tca gac ctg ttg ata gat gaa aac tgt ttg		672
Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu		
210 215 220		
ctt tct cct ctg gcg gga gaa gac gat tca ttc ctt ttg gaa gga aac		720
Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn		
225 230 235 240		
tcg aat gag gac tgc aag cct ctc att tta ccg gac act aaa ccc aaa		768
Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys		
245 250 255		
att aag gat aat gga gat ctg gtt ttg tca agc ccc agt aat gta aca		816
Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr		
260 265 270		
ctg ccc caa gtg aaa aca gaa aaa gaa gat ttc atc gaa ctc tgc acc		864
Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr		
275 280 285		
cct ggg gta att aag caa gag aaa ctg ggc aca gtt tac tgt cag gca		912
Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala		
290 295 300		
agc ttt cct gga gca aat ata att ggt aat aaa atg tct gcc att tct		960
Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser		
305 310 315 320		
gtt cat ggt gtg agt acc tct gga gga cag atg tac cac tat gac atg		1008
Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met		
325 330 335		

aat aca gca tcc ctt tct caa cag cag gat cag aag cct att ttt aat		1056	
Asn Thr Ala Ser Leu Ser Gln Gln Asp Gln Lys Pro Ile Phe Asn			
340	345	350	
gtc att cca cca att ccc gtt ggt tcc gaa aat tgg aat agg tgc caa		1104	
Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln			
355	360	365	
gga tct gga gat gac aac ttg act tct ctg ggg act ctg aac ttc cct		1152	
Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro			
370	375	380	
ggc cga aca gtt ttt tct aat ggc tat tca agc ccc agc atg aga cca		1200	
Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro			
385	390	395	400
gat gta agc tct cct cca tcc agc tcc tca aca gca aca aca gga cca		1248	
Asp Val Ser Ser Pro Pro Ser Ser Ser Thr Ala Thr Thr Gly Pro			
405	410	415	
cct ccc agc ggc cgc gtg caa gag gag ctg tgc ctg gtt tgc ggc gac		1296	
Pro Pro Ser Gly Arg Val Gln Glu Glu Leu Cys Leu Val Cys Gly Asp			
420	425	430	
agg gcc tcc ggc tac cac tac aac gcc ctc acc tgt gga tcc tgc aag		1344	
Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Gly Ser Cys Lys			
435	440	445	
gtg ttc ttt cga cgc agc gtt acg aag agc gcc gtc tac tgc tgc aag		1392	
Val Phe Phe Arg Arg Ser Val Thr Lys Ser Ala Val Tyr Cys Cys Lys			
450	455	460	
tcc ggg cgc gcc tgc gaa atg gac atg tac atg agg cga aag tgt cag		1440	
Phe Gly Arg Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys Cys Gln			
465	470	475	480
gag tgc cgc ctg aaa aag tgc ctg gcc gtg ggt atg cgg ccg gaa tgc		1488	
Glu Cys Arg Leu Lys Cys Leu Ala Val Gly Met Arg Pro Glu Cys			
485	490	495	
gtc gtc ccg gag aac caa tgt gcg atg aag cgg cgc gaa aag aag gcc		1536	
Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys Lys Ala			
500	505	510	
cag aag gag aag gac aaa atg acc act tcg ccg agc tct cag cat ggc		1584	
Gln Lys Glu Lys Asp Lys Met Thr Thr Ser Pro Ser Ser Gln His Gly			
515	520	525	
ggc aat ggc agc ttg gcc tct ggt ggc ggc caa gac ttt gtt aag aag		1632	
Gly Asn Gly Ser Leu Ala Ser Gly Gly Gln Asp Phe Val Lys Lys			
530	535	540	
gag att ctt gac ctt atg aca tgc gag ccg ccc cag cat gcc act att		1680	
Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Gln His Ala Thr Ile			
545	550	555	560

ccg cta cta cct gat gaa ata ttg gcc aag tgt caa gcg cgc aat ata Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys Gln Ala Arg Asn Ile 565	570	575	1728	
cct tcc tta acg tac aat cag ttg gcc gtt ata tac aag tta att tgg Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val Ile Tyr Lys Leu Ile Trp 580	585	590	1776	
tac cag gat ggc tat gag cag cca tct gaa gag gat ctc agg cgt ata Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Arg Arg Ile 595	600	605	1824	
atg agtcaa ccc gat gag aac gag agc caa acg gac gtc agc ttt cgg Met Ser Gln Pro Asp Glu Asn Glu Ser Gln Thr Asp Val Ser Phe Arg 610	615	620	1872	
cat ata acc gag ata acc ata ctc acg gtc cag ttg att gtt gag ttt His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe 625	630	635	640	1920
gct aaa ggt cta cca gcg ttt aca aag ata ccc cag gag gac cag atc Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile 645	650	655	1968	
acg tta cta aag gcc tgc tcg gag gtg atg atg ctg cgt atg gca Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Met Ala 660	665	670	2016	
cga cgc tat gac cac agc tcg gac tca ata ttc ttc gcg aat aat aga Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg 675	680	685	2064	
tca tat acg cgg gat tct tac aaa atg gcc gga atg gct gat aac att Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile 690	695	700	2112	
gaa gac ctg ctg cat ttc tgc cgc caa atg ttc tcg atg aag gtg gac Glu Asp Leu Leu His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp 705	710	715	720	2160
aac gtc gaa tac gcg ctt ctc act gcc att gtg atc ttc tcg gac cgg Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg 725	730	735	2208	
ccg ggc ctg gag aag gcc caa cta gtc gaa gcg atc cag agc tac tac Pro Gly Leu Glu Lys Ala Gln Leu Val Glu Ala Ile Gln Ser Tyr Tyr 740	745	750	2256	
atc gac acg cta cgc att tat ata ctc aac cgc cac tgc ggc gac tca Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His Cys Gly Asp Ser 755	760	765	2304	
atg agc ctc gtc ttc tac gca aag ctg ctc tcg atc ctc acc gag ctg Met Ser Leu Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu 770	775	780	2352	

cg t acg ctg ggc aac cag aac gcc gag atg tgt ttc tca cta aag ctc		2400
Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu		
785 790 795 800		
aaa aac cgc aaa ctg ccc aag ttc ctc gag gag atc tgg gac gtt cat		2448
Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His		
805 810 815		
gcc atc ccg cca tcg gtc cag tcg cac ctt cag att acc cag gag gag		2496
Ala Ile Pro Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu		
820 825 830		
aac gag cgt ctc gag cgg gct gag cgt atg cgg gca tcg gtt ggg ggc		2544
Asn Glu Arg Leu Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly		
835 840 845		
gcc att acc gcc ggc att gat tgc gac tct gcc tcc act tcg gcg gcg		2592
Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala		
850 855 860		
gca gcc gcg gcc cag cat cag cct cag cct cag ccc cag ccc caa ccc		2640
Ala Ala Ala Ala Gln His Gln Pro Gln Pro Gln Pro Gln Pro Gln Pro		
865 870 875 880		
tcc tcc ctg acc cag aac gat tcc cag cac cag aca cag ccg cag cta		2688
Ser Ser Leu Thr Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu		
885 890 895		
caa cct cag cta cca cct cag ctg caa ggt caa ctg caa ccc cag ctc		2736
Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu		
900 905 910		
caa cca cag ctt cag acg caa ctc cag cca cag att caa cca cag cca		2784
Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro		
915 920 925		
cag ctc ctt ccc gtc tcc gct ccc gtg ccc gcc tcc gta acc gca cct		2832
Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro		
930 935 940		
gg tcc ttg tcc gcg gtc agt acg agc agc gaa tac atg ggc gga agt		2880
Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser		
945 950 955 960		
g cg gcc ata gga ccc atc acg ccg gca acc acc agc agt atc acg gct		2928
Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala		
965 970 975		
gcc gtt acc gct agc tcc acc aca tca gcg gta ccg atg ggc aac gga		2976
Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly		
980 985 990		
gtt gga gtc ggt gtt ggg gtg ggc ggc aac gtc agc atg tat gcg aac		3024
Val Gly Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn		
995 1000 1005		

gcc cag acg gcg atg gcc ttg atg ggt gta gcc ctg cat tcg cac caa		3072
Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln		
1010	1015	1020
gag cag ctt atc ggg gga gtg gcg gtt aag tcg gag cac tcg acg act		3120
Glu Gln Leu Ile Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr		
1025	1030	1035
1040		
gca tag		3126
Ala		

<210> 9  
<211> 1041  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Recombinant  
GECR

<400> 9			
Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser			
1	5	10	15
Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr			
20	25	30	
Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu			
35	40	45	
Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp			
50	55	60	
Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys			
65	70	75	80
Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys			
85	90	95	
Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu			
100	105	110	
Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn			
115	120	125	
Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser			
130	135	140	
Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His			
145	150	155	160
Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr			
165	170	175	
Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp			
180	185	190	

Ile	Leu	Gln	Asp	Leu	Glu	Phe	Ser	Ser	Gly	Ser	Pro	Gly	Lys	Glu	Thr
195							200						205		
Asn	Glu	Ser	Pro	Trp	Arg	Ser	Asp	Leu	Leu	Ile	Asp	Glu	Asn	Cys	Leu
210								215					220		
Leu	Ser	Pro	Leu	Ala	Gly	Glu	Asp	Asp	Ser	Phe	Leu	Leu	Glu	Gly	Asn
225							230			235			240		
Ser	Asn	Glu	Asp	Cys	Lys	Pro	Leu	Ile	Leu	Pro	Asp	Thr	Lys	Pro	Lys
245							250						255		
Ile	Lys	Asp	Asn	Gly	Asp	Leu	Val	Leu	Ser	Ser	Pro	Ser	Asn	Val	Thr
260							265						270		
Leu	Pro	Gln	Val	Lys	Thr	Glu	Lys	Glu	Asp	Phe	Ile	Glu	Leu	Cys	Thr
275							280						285		
Pro	Gly	Val	Ile	Lys	Gln	Glu	Lys	Leu	Gly	Thr	Val	Tyr	Cys	Gln	Ala
290							295						300		
Ser	Phe	Pro	Gly	Ala	Asn	Ile	Ile	Gly	Asn	Lys	Met	Ser	Ala	Ile	Ser
305							310			315			320		
Val	His	Gly	Val	Ser	Thr	Ser	Gly	Gly	Gln	Met	Tyr	His	Tyr	Asp	Met
325							330						335		
Asn	Thr	Ala	Ser	Leu	Ser	Gln	Gln	Asp	Gln	Lys	Pro	Ile	Phe	Asn	
340							345						350		
Val	Ile	Pro	Pro	Ile	Pro	Val	Gly	Ser	Glu	Asn	Trp	Asn	Arg	Cys	Gln
355							360						365		
Gly	Ser	Gly	Asp	Asp	Asn	Leu	Thr	Ser	Leu	Gly	Thr	Leu	Asn	Phe	Pro
370							375						380		
Gly	Arg	Thr	Val	Phe	Ser	Asn	Gly	Tyr	Ser	Ser	Pro	Ser	Met	Arg	Pro
385							390			395			400		
Asp	Val	Ser	Ser	Pro	Pro	Ser	Ser	Ser	Thr	Ala	Thr	Thr	Gly	Pro	
405							410						415		
Pro	Pro	Ser	Gly	Arg	Val	Gln	Glu	Glu	Leu	Cys	Leu	Val	Cys	Gly	Asp
420							425						430		
Arg	Ala	Ser	Gly	Tyr	His	Tyr	Asn	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys
435							440						445		
Val	Phe	Phe	Arg	Arg	Ser	Val	Thr	Lys	Ser	Ala	Val	Tyr	Cys	Cys	Lys
450							455						460		
Phe	Gly	Arg	Ala	Cys	Glu	Met	Asp	Met	Tyr	Met	Arg	Arg	Lys	Cys	Gln
465							470			475			480		
Glu	Cys	Arg	Leu	Lys	Lys	Cys	Leu	Ala	Val	Gly	Met	Arg	Pro	Glu	Cys
485							490						495		

Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys Lys Ala  
 500 505 510

Gln Lys Glu Lys Asp Lys Met Thr Thr Ser Pro Ser Ser Gln His Gly  
 515 520 525

Gly Asn Gly Ser Leu Ala Ser Gly Gly Gln Asp Phe Val Lys Lys  
 530 535 540

Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Gln His Ala Thr Ile  
 545 550 555 560

Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys Gln Ala Arg Asn Ile  
 565 570 575

Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val Ile Tyr Lys Leu Ile Trp  
 580 585 590

Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Arg Arg Ile  
 595 600 605

Met Ser Gln Pro Asp Glu Asn Glu Ser Gln Thr Asp Val Ser Phe Arg  
 610 615 620

His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe  
 625 630 635 640

Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile  
 645 650 655

Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Met Ala  
 660 665 670

Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg  
 675 680 685

Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile  
 690 695 700

Glu Asp Leu Leu His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp  
 705 710 715 720

Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg  
 725 730 735

Pro Gly Leu Glu Lys Ala Gln Leu Val Glu Ala Ile Gln Ser Tyr Tyr  
 740 745 750

Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His Cys Gly Asp Ser  
 755 760 765

Met Ser Leu Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu  
 770 775 780

Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu  
 785 790 795 800

Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His  
 805 810 815

Ala Ile Pro Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu  
 820 825 830

Asn Glu Arg Leu Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly  
 835 840 845

Ala Ile Thr Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala  
 850 855 860

Ala Ala Ala Ala Gln His Gln Pro Gln Pro Gln Pro Gln Pro Gln Pro  
 865 870 875 880

Ser Ser Leu Thr Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu  
 885 890 895

Gln Pro Gln Leu Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu  
 900 905 910

Gln Pro Gln Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro  
 915 920 925

Gln Leu Leu Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro  
 930 935 940

Gly Ser Leu Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser  
 945 950 955 960

Ala Ala Ile Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala  
 965 970 975

Ala Val Thr Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly  
 980 985 990

Val Gly Val Gly Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn  
 995 1000 1005

Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln  
 1010 1015 1020

Glu Gln Leu Ile Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr  
 1025 1030 1035 1040

Ala

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<211> 17
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<220>
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<223> a, c, t, g, other or unknown

<220>
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<222> (7)..(11)
<223> a, c, t, g, other or unknown, wherein the length of this
      region may vary in length from 0 to 5, with 1 being
      especially preferred

<220>
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17

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<210> 11
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<220>
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17

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<213> Artificial Sequence

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<220>  
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13

<210> 13  
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49

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<212> DNA  
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